Blast 2 Sequences results

PubMed Entrez BLAST OMIM Taxonomy Structure

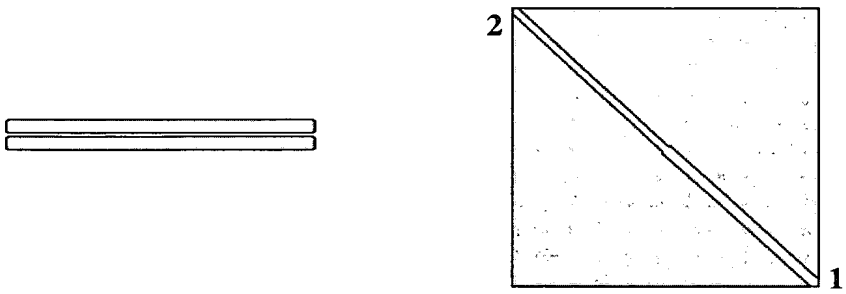
BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.6 [Apr-09-2003]

Match: 1 Mismatch: -2 gap open: 5 gap extension: 2

x_dropoff: 50 expect: 10.000 wordsize: 11 Filter ☐ Align

Sequence 1 lcl|60/054,212 SIN:4 **Length** 955 (1 .. 955)

Sequence 2 lcl|09/820,649 SIN:12 **Length** 955 (1 .. 955)



NOTE:The statistics (bitscore and expect value) is calculated based on the size of nr database.

NOTE:If protein translation is reversed, please repeat the search with reverse strand of the query sequence

```
Score = 1836 bits (955), Expect = 0.0
Identities = 955/955 (100%)
 Strand = Plus / Minus
```

```
Query: 1   tcgagttttttttttttttttgttttatggcatttgtttctttattgaaaatatttg 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 955 tcgagttttttttttttttttgttttatggcatttgtttctttattgaaaatatttg 896

Query: 61  tcttcttgcattagaacacaagcattgtggatggcagagacttgactgttcacatctgta 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 895 tcttcttgcattagaacacaagcattgtggatggcagagacttgactgttcacatctgta 836

Query: 121 tctgctggaatacttattaaatggatgagtaactccttaggccagtgtcagcattgctgt 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 835 tctgctggaatacttattaaatggatgagtaactccttaggccagtgtcagcattgctgt 776

Query: 181 catcccaggacctacctttggtcccatacaagtagaagaagtcacagtagaagatggttt 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 775 catcccaggacctacctttggtcccatacaagtagaagaagtcacagtagaagatggttt 716

Query: 241 gtactactccagacacgactgcaatttggtcatagaaattctcagtctggtaccgcctga 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 715 gtactactccagacacgactgcaatttggtcatagaaattctcagtctggtaccgcctga 656

Query: 301 tccagttagccaggtagagtgcccggtacagacccagaaagaacaggtagtgagtagtta 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 655 tccagttagccaggtagagtgcccggtacagacccagaaagaacaggtagtgagtagtta 596
```

```
Query: 361 tggtctcagcctctccagtcttgctgatcatgaagagctggggcaggatagccactgatt 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 595 tggtctcagcctctccagtcttgctgatcatgaagagctggggcaggatagccactgatt 536


Query: 421 ccagatagatagagaaagtccagaggatctccagcagagtgaaactgtagttttcaagga 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 535 ccagatagatagagaaagtccagaggatctccagcagagtgaaactgtagttttcaagga 476


Query: 481 aggaaaggccaatgactgggaccagaagaaactccaggcggaatgtgtcattctcactgt 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 475 aggaaaggccaatgactgggaccagaagaaactccaggcggaatgtgtcattctcactgt 416


Query: 541 caaaagttttacggaatttcccatatatcatgtacactgtaacataggcacagaggagaa 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 415 caaaagttttacggaatttcccatatatcatgtacactgtaacataggcacagaggagaa 356


Query: 601 aaaccaccttcattactgtgttgtagatggagatgaagttggtgaacaggtccaggtacc 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 355 aaaccaccttcattactgtgttgtagatggagatgaagttggtgaacaggtccaggtacc 296


Query: 661 tggtggtgaagacgagagcaaacaggatctggctcttcccagagatgcccttgcagcact 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 295 tggtggtgaagacgagagcaaacaggatctggctcttcccagagatgcccttgcagcact 236


Query: 721 tggacctccagatcttccccagcagcaagatcatggccaggaggtggctcaggtcgccga 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 235 tggacctccagatcttccccagcagcaagatcatggccaggaggtggctcaggtcgccga 176


Query: 781 ggattcggaacacgttcatggtccagccagtcagtcgtgcgcccgcgcccagcaaacttc 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 175 ggattcggaacacgttcatggtccagccagtcagtcgtgcgcccgcgcccagcaaacttc 116


Query: 841 taggaaactttctggcgggcagggcggctgccacgtctccggccccggtctctaggtgcc 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 115 taggaaactttctggcgggcagggcggctgccacgtctccggccccggtctctaggtgcc 56


Query: 901 ccagagccctgcctgcgcctcacagctccgcgatcgcacccgcgcgccgccgccc 955
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 55  ccagagccctgcctgcgcctcacagctccgcgatcgcacccgcgcgccgccgccc 1

CPU time:     0.01 user secs.       0.01 sys. secs          0.02 total secs.

Lambda      K      H
    1.33     0.621     1.12

Gapped
Lambda      K      H
    1.33     0.621     1.12


Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 16
Number of Sequences: 0
Number of extensions: 16
Number of successful extensions: 15
Number of sequences better than 10.0: 1
```

Number of HSP's better than 10.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 1
length of query: 955
length of database: 10,130,642,339
effective HSP length: 25
effective length of query: 930
effective length of database: 10,130,642,314
effective search space: 9421497352020
effective search space used: 9421497352020
T: 0
A: 0
X1: 6 (11.5 bits)
X2: 26 (50.0 bits)
S1: 12 (23.8 bits)
S2: 21 (41.1 bits)